#4

SEQUENCE LISTING

<110> Bowdish, Katherine S.
Frederickson, Shana
Renshaw, Mark

<120> RATIONALLY DESIGNED ANTIBODIES

<130> 1087-2

<140> 10/006,593
<141> 2001-12-05

<150> US 60/251,448
<151> 2000-12-05

<150> US 60/288,889
<151> 2001-05-04

<150> US 60/294,068
<151> 2001-05-29

<160> 118

<170> PatentIn version 3.1

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<220>
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Asp Tyr His Cys Arg Met Gly Pro Leu Thr Trp Val Cys Lys Pro Leu
1 5 10 15

Gly Gly

<210> 4
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<400> 4

Gly Asp Thr Ile Phe Gly Val Thr Met Gly Tyr Tyr Ala Met Asp Val
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<210> 9
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<210> 14
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<210> 16
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<220>
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ggccatggct ggttgggcag c 21

<210> 19
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ggc 63

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<223> n is a, c, g or t

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gtc 63

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atc 63

<210> 24
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gtg 63

<210> 25
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<220>
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<400> 25

Pro Pro Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Gly Gly

<210> 26
<211> 54
<212> DNA
<213> artificial sequence

<220>
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<400> 26
ccgcccattg aagggccgac gctgcggcaa tggctggcgg cgcgcgcggg aggc 54

<210> 27
<211> 18
<212> PRT
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<220>
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<400> 27

Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Gly Gly

<210> 28
<211> 54
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<220>
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<400> 28
ggggtattg aagggccgac gctgcggcaa tggctggcgg cgcgcgcggg cgga 54

<210> 29
<211> 18
<212> PRT
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<220>
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<400> 29

Gly Gly Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Gly Gly

<210> 30
<211> 54
<212> DNA
<213> artificial sequence

<220>
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<400> 30
ggcggtattg aagggccgac gctgcggcaa tggctggcgg cgcgcgcggg aggc 54

<210> 31
<211> 18

<212> PRT
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<220>
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<400> 31

Trp Leu Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Pro Val

<210> 32
<211> 54
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<220>
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tggctgattg aagggccgac gctgcggcaa tggctggcgg cgcgcgcgcc tgtc 54

<210> 33
<211> 18
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<220>
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<400> 33

Met Ile Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Val Gly

<210> 34
<211> 54
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<220>
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<210> 35
<211> 18
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<220>
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<400> 35

Val Val Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Pro Val

<210> 36
<211> 54
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<210> 37
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<220>
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<400> 37

Gly Pro Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Pro Asp

<210> 38
<211> 54
<212> DNA
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<220>
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<210> 39
<211> 18
<212> PRT
<213> artificial sequence

<220>
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<400> 39

Leu Pro Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Pro Val

<210> 40
<211> 54
<212> DNA
<213> artificial sequence

<220>
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<400> 40
ttgccaattg aagggccgac gctgcggcaa tggctggcgg cgcgcgcgcc tgtt 54

<210> 41
<211> 18
<212> PRT
<213> artificial sequence

<220>
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<400> 41

Ser Leu Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Pro Ile

<210> 42
<211> 54
<212> DNA
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<220>
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<400> 42
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<210> 43
<211> 18
<212> PRT
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<220>
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<400> 43

Thr Met Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Pro Val

<210> 44
<211> 54
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<210> 45
<211> 18
<212> PRT
<213> artificial sequence

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<400> 45

Thr Thr Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Pro Val

<210> 46
<211> 54

<212> DNA
<213> artificial sequence

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<210> 47
<211> 18
<212> PRT
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1 5 10 15

Cys Ser

<210> 48
<211> 54
<212> DNA
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<220>
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<210> 49
<211> 18
<212> PRT
<213> artificial sequence

<220>
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Gln Thr Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Pro Asp

<210> 50
<211> 54
<212> DNA
<213> artificial sequence

<220>
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cagacaattg aagggccgac gctgcggcaa tggctggcgg cgcgcgcgcc tcac 54

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<211> 60
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<220>
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<210> 52
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gaggaaaaag tgaaaaccct gaaagctcag aactccgagc tggcgtccac tgccaacatg 120

ctgcgcgaac aggtggcaca gctgaaacag aaagttatga accatggcgg ttgtgctagt 180

ggccaggccg gccagcacca tcaccatcac catggcgcat acccgtacga cgttccggac 240

tacgcttctt aggagggtgg tggctctgag 270

<210> 53
<211> 81
<212> PRT
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<220>
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<400> 53

Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Cys Gly Gly Arg Ile Ala
1 5 10 15

Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser Glu Leu
20 25 30

Ala Ser Thr Ala Asn Met Leu Arg Glu Gln Val Ala Gln Leu Lys Gln
35 40 45

Lys Val Met Asn His Gly Gly Cys Ala Ser Gly Gln Ala Gly Gln His
50 55 60

His His His His His Gly Ala Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
65 70 75 80

Ser

<210> 54
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<212> DNA
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<400> 54
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gtctcctgca gggcttctgg aggcaccttc aacaattatg ccatcagctg ggtgcgacag 120

gcccctggac aagggcttga gtggatggga gggatcttcc ctttccgtaa tacagcaaag 180

tacgcacaac acttccaggg cagagtcacc attaccgcgg acgaatccac gggcacagcc 240

tacatggagc tgagcagcct gagatctgag gacacggcca tatattattg tgcgagaggg 300

gatacgattt ttggagtgac catgggatac tacgctatgg acgtctgggg ccaagggacc 360

acggtcaccg tctccgcagc ctccaccaag ggcccatcgg tcttcccccct ggcaccctcc 420

tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 480

gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 540

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600

agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 660

gacaagaaag ttgagcccaa atcttgtgac aaaactagt 699

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caggctccca ggctcctcat ctatggtaca tccagcaggg ccactggcat cccagacagg 180

ttcagtggca gtgggtctgg gacagacttc actctcacca tcagcagact ggagcctgaa 240

gattttgcag tgtactactg tcagcagtat ggtggctcac cgtggttcgg ccaagggacc 300

aaggtggaac tcaaacgaac tgtggctgca ccatctgtct tcatcttccc gccatctgat 360

gagcagttga aatctggaac tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga 420

gaggccaaag tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt 480

gtcacagagc aggacagcaa ggacagcacc tacagcctca gcagcaccct gacgctgagc 540

aaagcagact acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc 600

ttgcccgtca caaagagctt caacagggga gagtgttagt tctaga 646

<210> 56
<211> 28
<212> PRT
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<223> Xaa is any of 14 amino acids

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<222> (22)..(23)
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Tyr Tyr Cys Ala Arg Xaa Xaa Ile Glu Gly Pro Thr Leu Arg Gln Trp
1 5 10 15

Leu Ala Ala Arg Ala Xaa Xaa Trp Gly Gln Gly Thr
20 25

<210> 57
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<212> DNA
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<223> n is a, c, g or t

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gcgnnynnyt ggggccaagg gacc 84

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<212> DNA
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<220>
<223> vector

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catttttaa ccaataggcc gaaatcggca aaatcccttа taaatcaaaa gaatagaccg 120

agatagggtt gagtgttgtt ccagtttgga acaagagtcc actattaaag aacgtggact 180

ccaacgtcaa agggcgaaaa accgtctatc agggcgatgg cccactacgt gaaccatcac 240

cctaatcaag ttttttgggg tcgaggtgcc gtaaagcact aaatcggaac cctaaaggga 300

gcccccgatt tagagcttga cggggaaagc cggcgaacgt ggcgagaaag gaagggaaga 360

aagcgaaagg agcgggcgct agggcgctgg caagtgtagc ggtcacgctg cgcgtaacca 420

ccacacccgc cgcgcttaat gcgccgctac agggcgcgtc aggtggcact tttcggggaa 480

atgtgcgcgg aacccctatt tgtttatttt tctaaataca ttcaaatatg tatccgctca 540

tgagacaata accctgataa atgcttcaat aatattgaaa aaggaagagt atgagtattc 600

aacatttccg tgtcgccctt attccctttt ttgcggcatt ttgccttcct gtttttgctc 660

acccagaaac gctggtgaaa gtaaaagatg ctgaagatca gttgggtgca cgagtgggtt 720

acatcgaact ggatctcaac agcggtaaga tccttgagag ttttcgcccc gaagaacgtt 780

ttccaatgat gagcactttt aaagttctgc tatgtggcgc ggtattatcc cgtattgacg 840

ccgggcaaga gcaactcggt cgccgcatac actattctca gaatgacttg gttgagtact 900

caccagtcac agaaaagcat cttacggatg gcatgacagt aagagaatta tgcagtgctg 960

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aaccggagct gaatgaagcc ataccaaacg acgagctgta caccacgatg cctgtagcaa 1140

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cgtttctttt atatgttgcc acctttatgt atgtattttc tacgtttgct aacatactgc 5100

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<210> 61
<211> 18
<212> PRT
<213> artificial sequence

<220>

<223> TPO mimetic with flanking amino acids

<400> 61

Asn Pro Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Arg Gly

<210> 62
<211> 41
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 62
taggatgcgg ccgcacaggt ctttttttt ttttttttt t 41

<210> 63
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 63
ccatgtaggc tgtgcccgtg gatt 24

<210> 64
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 64
ccacgggcac agcctacatg gagc 24

<210> 65
<211> 54
<212> DNA
<213> artificial sequence

<220>
<223> nucleic acid encoding TPO mimetic peptide flanking sequence

<400> 65

ttgccaattg aagggccgac gctgcggcaa tggctggcgg cgcgcgcgcc tgtt 54

<210> 66
<211> 18
<212> PRT
<213> artificial sequence

<220>
<223> TPO mimetic peptide with flanking sequence

<400> 66

Leu Pro Ile Glu Gly Pro Thr Leu Arg Gln Trp Leu Ala Ala Arg Ala
1 5 10 15

Pro Val

<210> 67
<211> 472
<212> PRT
<213> artificial sequence

<220>
<223> Humanized antibody heavy chain

<400> 67

Met Lys Trp Ser Trp Val Ile Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe
35 40 45

Ser Asn Tyr Trp Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Glu Trp Met Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Glu Tyr Thr
65 70 75 80

Glu Asn Phe Lys Asp Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
85 90 95

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

```
Tyr Tyr Cys Ala Arg Leu Pro Ile Glu Gly Pro Thr Leu Arg Gln Trp
        115                 120                 125

Leu Ala Ala Arg Ala Pro Val Trp Gly Gln Gly Thr Leu Val Thr Val
    130                 135                 140

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
145                 150                 155                 160

Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys
                165                 170                 175

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
            180                 185                 190

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
        195                 200                 205

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr
    210                 215                 220

Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val
225                 230                 235                 240

Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
                245                 250                 255

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
            260                 265                 270

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
        275                 280                 285

Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
    290                 295                 300

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
305                 310                 315                 320

Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                325                 330                 335
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Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
            340                 345                 350

Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        355                 360                 365

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
    370                 375                 380

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
385                 390                 395                 400

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                405                 410                 415

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            420                 425                 430

Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
        435                 440                 445

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    450                 455                 460

Ser Leu Ser Leu Ser Leu Gly Lys
465                 470
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<210> 68
<211> 1419
<212> DNA
<213> artificial sequence

<220>
<223> nucleic acid encoding humanized antibody heavy chain

<400> 68

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gtccaactgg tgcaatccgg cgccgaggtc aagaagccag gggcctcagt caaagtgtcc    120

tgtaaagcta gcggctatat tttttctaat tattggattc aatgggtgcg tcaggccccc    180

gggcagggcc tggaatggat gggtgagatc ttaccgggct ctggtagcac cgaatatacc    240

gaaaatttta aagaccgtgt tactatgacg cgtgacactt cgactagtac agtatacatg    300

gagctctcca gcctgcgatc ggaggacacg gccgtctatt attgcgcgcg tttgccaatt    360
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gaagggccga cgctgcggca atggctggcg gcgcgcgcgc ctgtttgggg tcaaggaacc 420

ctggtcactg tctcgagcgc ctccaccaag ggcccatccg tcttcccccc ggcgccctgc 480

tccaggagca cctccgagag cacagccgcc ctgggctgcc tggtcaagga ctacttcccc 540

gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 600

gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 660

aacttcggca cccagaccta cacctgcaac gtagatcaca agcccagcaa caccaaggtg 720

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gcaggaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg 840

acccctgagg tcacgtgcgt ggtggtggac gtgagccagg aagaccccga ggtccagttc 900

aactggtacg tggatggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 960

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cccgtgctgg actccgacgg ctccttcttc ctctacagca ggctaaccgt ggacaagagc 1320

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tacacacaga agagcctctc cctgtctctg ggtaaatga 1419

<210> 69
<211> 236
<212> PRT
<213> artificial sequence

<220>
<223> Humanized antibody light chain

<400> 69

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gly Ala Ser
35 40 45

Glu Asn Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
50 55 60

Ala Pro Lys Leu Leu Ile Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Asn
100 105 110

Val Leu Asn Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
115 120 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
130 135 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145 150 155 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
165 170 175

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
180 185 190

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
195 200 205

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
210 215 220

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 70
<211> 711
<212> DNA
<213> artificial sequence

<220>
<223> nucleic acid encoding humanized antibody light chain

<400> 70
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gtcaccatca cctgcggcgc cagcgaaaac atctatggcg cgctgaactg gtatcaacag 180

aaacccggga aagctccgaa gcttctgatt tacggtgcga cgaacctggc agatggagtc 240

ccttctcgct tctctggatc cggctccgga acggatttca ctctgaccat cagcagtctg 300

cagcctgaag acttcgctac gtattactgt cagaacgttt taaatactcc gttgactttc 360

ggacagggta ccaaggtgga aataaaacga actgtggctg caccatctgt cttcatcttc 420

ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 480

ttctatccca gagaggccaa agtacagtgg aaggtggata acgccctcca atcgggtaac 540

tcccaggaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagcacc 600

ctgacgctga gcaaagcaga ctacgagaaa cacaaagtct acgcctgcga agtcacccat 660

cagggcctga gctcgcccgt cacaaagagc ttcaacaggg gagagtgtta g 711

<210> 71
<211> 22
<212> PRT
<213> artificial sequence

<220>
<223> EPO mimetic with random flanking amino acids

<220>
<221> MISC_FEATURE
<222> (1)..(2)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is any amino acid

<220>
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<223> Xaa is any amino acid

<220>

<221> MISC_FEATURE
<222> (21)..(22)
<223> Xaa is any amino acid

<400> 71

Xaa Xaa Asp Tyr His Xaa Arg Met Gly Pro Leu Thr Trp Val Xaa Lys
1 5 10 15

Pro Leu Gly Gly Xaa Xaa
20

<210> 72
<211> 21
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 72
taggatgcgg ccgcacaggt c 21

<210> 73
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 73
cacgcgcaca acacgtctag aracatccag atgacccag 39

<210> 74
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 74
cacgcgcaca acacgtctag agmcatccag ttgacccag 39

<210> 75
<211> 39
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<213> artificial sequence

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<223> primer

<400> 75
cacgcgcaca acacgtctag agccatccrg atgacccag 39

<210> 76
<211> 39
<212> DNA
<213> artificial sequence

<220>
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<400> 76
cacgcgcaca acacgtctag agtcatctgg atgacccag 39

<210> 77
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 77
cacgcgcaca acacgtctag agatattgtg atgacccag 39

<210> 78
<211> 39
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<220>
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<400> 78
cacgcgcaca acacgtctag agatrttgtg atgactcag 39

<210> 79
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cacgcgcaca acacgtctag agaaattgtg ttgacrcag 39

<210> 80
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<220>
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<400> 80
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<210> 81
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<400> 81
cacgcgcaca acacgtctag agaaattgta atgacacag 39

<210> 82
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cacgcgcaca acacgtctag agacatcgtg atgacccag 39

<210> 83
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<400> 83
cacgcgcaca acacgtctag agaaacgaca ctcacgcag 39

<210> 84
<211> 39
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<220>
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<400> 84
cacgcgcaca acacgtctag agaaattgtg ctgactcag 39

<210> 85
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<220>
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<400> 85
cacgcgcaca acacgtctag agatgttgtg atgacacag 39

<210> 86
<211> 22
<212> DNA
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<220>
<223> primer

<400> 86
attaatacga ctcactatag gg 22

<210> 87
<211> 20
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 87
aattaaccct cactaaaggg 20

<210> 88
<211> 59
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 88
agccagccac tggcgcaggg ttgggccttc gatcgggttc ctgatgagga gctttggrg 59

<210> 89
<211> 59
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 89

agccagccac tggcgcaggg ttgggccttc gatcgggttt tgaataatga aaatagcag 59

<210> 90
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<212> DNA
<213> artificial sequence

<220>
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<400> 90
agccagccac tggcgcaggg ttgggccttc gatcgggttg taaatgagca rcttaggag 59

<210> 91
<211> 59
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 91
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<210> 92
<211> 59
<212> DNA
<213> artificial sequence

<220>
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<400> 92
agccagccac tggcgcaggg ttgggccttc gatcgggtta taaattaggc gccttggag 59

<210> 93
<211> 59
<212> DNA
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<220>
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<400> 93
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<210> 94
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<220>
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<210> 99
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<213> artificial sequence

<220>
<223> primer

<400> 99
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<210> 100
<211> 59
<212> DNA
<213> artificial sequence

<220>
<223> primer

<400> 100
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<210> 101
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<212> DNA
<213> artificial sequence

<220>
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<400> 101
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<210> 102
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<400> 108
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agatagggtt gagtgttgtt ccagtttgga acaagagtcc actattaaag aacgtggact 180

ccaacgtcaa agggcgaaaa accgtctatc agggcgatgg cccactacgt gaaccatcac 240

cctaatcaag ttttttgggg tcgaggtgcc gtaaagcact aaatcggaac cctaaaggga 300

gcccccgatt tagagcttga cggggaaagc cggcgaacgt ggcgagaaag gaagggaaga 360

aagcgaaagg agcgggcgct agggcgctgg caagtgtagc ggtcacgctg cgcgtaacca 420

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<220>
<223> part of mimetic

<400> 112

Gly Pro Thr Leu Arg Gln Trp Leu
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<210> 113
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<220>
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<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is any amino acid

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is any amino acid

<400> 113

Gly Xaa Gly Pro Thr Leu Arg Gln Trp Leu Xaa Tyr Ala Gln Lys Phe
1 5 10 15

Gln Gly

<210> 114
<211> 48
<212> DNA
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<220>
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<220>
<221> misc_feature
<222> (26)..(27)
<223> n is a, c, g or t

<400> 114
cagccactgg cgcagggttg ggccmnnccc tcccatccac tcaagccc 48

<210> 115
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<212> DNA
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<220>
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<220>
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<222> (25)..(26)
<223> n is a, c, g or t

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<210> 116
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<400> 116
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gggaaagctc ctaagctcct gatctataac ccgatcgaag gcccaaccct gcgccagtgg 180

ctggctactc gcgctcgtgg tggggtccca tcaaggttca gcggcagtgg atctgggaca 240

gatttcactc tcaccatcag cagcctgcag cctgaagatt ttgcaactta ttactgccaa 300

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<400> 117

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
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Ser Ser Val Lys Val Ser Cys Arg Ala Ser Gly Gly Thr Phe Asn Asn
20 25 30

Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
35 40 45

Met Gly Gly Ile Phe Pro Phe Arg Asn Thr Ala Lys Tyr Ala Gln His
50 55 60

Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Gly Thr Ala
65 70 75 80

Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr
85 90 95

Cys Ala Arg Gly Asp Thr Ile Phe Gly Val Thr Met Gly Tyr Tyr Ala
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ala Ala Ser
115 120 125

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
130 135 140

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
145 150 155 160

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
165 170 175

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
180 185 190

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
195 200 205

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
210 215 220

Glu Pro Lys Ser Cys Asp Lys Thr Ser
225 230

<210> 118
<211> 212
<212> PRT
<213> human

<400> 118

Glu Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg
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Ala Thr Leu Ser Cys Arg Ala Ser His Ser Val Ser Arg Ala Tyr Leu
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Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Gly Thr Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65 70 75 80

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Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Pro Trp Phe
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Gly Gln Gly Thr Lys Val Glu Leu Lys Arg Thr Val Ala Ala Pro Ser
            100                 105                 110

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
        115                 120                 125

Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
    130                 135                 140

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
145                 150                 155                 160

Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
                165                 170                 175

Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys
            180                 185                 190

Glu Val Thr His Gln Gly Leu Ser Leu Pro Val Thr Lys Ser Phe Asn
        195                 200                 205

Arg Gly Glu Cys
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